

Appl. No. : 09/845,849  
Filed : APRIL 30, 2001

### AMENDMENTS TO THE SPECIFICATION

Please amend the first paragraph at page 1, line 1 of the specification as follows:

21 ~~"This application claims the benefit of priority from~~ is a divisional of Application Serial No. 09/060,726, filed on April 15, 1998, now U.S. Patent No. 6,225,530, all of which is hereby incorporated by reference in its entirety."

Please amend the two paragraphs at page 6, lines 11-16 of the specification as follows:

"FIG. 2 shows nucleotide sequences of FT cDNA inserts used for the sense and antisense constructs (pSKI059 (SEQ ID NO:1 ~~5~~) and pSKI060 (SEQ ID NO:3). For the sense strand the conceptual translation of the FT protein is shown in three-letter code under the DNA sequence. Vector sequences are underlined.

32 FIG. 3(A-C) shows sequence comparison of FT to related proteins in plants and mammals, with one-letter amino acid code. Figure 3(A) shows a comparison of At FT (SEQ ID NO:4), At TFL1 (SEQ ID NO:5), At E12A11 (SEQ ID NO:6), and Rn HNCP (SEQ ID NO:7). Figure 3(B) shows a phylogenetic tree of Am CEN, At TFL1, At FT, At E12A11 and Rn HNCP. Figure 3(C) shows alignment of peptide sequences of At FT (SEQ ID NO:8), At TFL1 (SEQ ID NO:9), Am CEN (SEQ ID NO:10), At E12A 11 (SEQ ID NO:11), Rn HNCP (SEQ ID NO: 12); and Hs HNCP (SEQ ID NO:13)."

Please remove the hand markings from the last paragraph beginning at page 7, line 21 so that it reads as follows:

33 "The invention provides a substantially purified flowering locus T (FT) polypeptide and polynucleotides encoding FT. FT of the invention is characterized as having a molecular weight of approximately 20 kD, as determined by SDS-PAGE, being located on chromosome 1 of Arabidopsis, and functioning to modulate flowering time."

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Please remove the hand markings and amend the paragraph from page 8, lines 9-21 of the specification as follows:

By "The invention includes polypeptides having substantially the same amino acid sequence as the amino acid sequence set forth in SEQ ID NO:2 or functional fragments thereof, or amino acid sequences that are substantially identical to SEQ ID NO:2. By "substantially the same" or "substantially identical" is meant a polypeptide or nucleic acid exhibiting at least 80%, preferably 85%, more preferably 90%, and most preferably 95% homology to a reference amino acid or nucleic acid sequence. For polypeptides, the length of comparison sequences will generally be at least 16 amino acids, preferably at least 20 amino acids, more preferably at least 25 amino acids, and most preferably 35 amino acids. For nucleic acids, the length of comparison sequences will generally be at least 50 nucleotides, preferably at least 60 nucleotides, more preferably at least 75 nucleotides, and most preferably 110 nucleotides. FT homologs having substantially the same sequence as FT can be identified using the phylogenetic tree as shown in FIG. 3B, for example. FT homologs would map closer to FT than to TFL1/CEN, for example."